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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=10; hr=10; min=20; sec=26; ms=768;]

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Reviewer Comments:

<210> 696
<211> 160
<212> PRT
<213> Homo sapiens
<220>
<221> MOD_RES
<222> (95)
<223> Variable amino acid
<220>
<221> MOD_RES
<222> (105)
<223> Variable amino acid
<220>
<221> MOD_RES
<222> (118)
<223> Variable amino acid
<220>
<221> MOD_RES
<222> (120)
<223> Variable amino acid
<400> 696

Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly
1					5				10					15	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
					20				25					30	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln
					35			40					45		
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
					50			55					60		

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr				
65	70	75		80
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Xaa				
	85	90		95
Gly Lys Glu Tyr Lys Cys Lys Val Ser Xaa Lys Gly Leu Pro Ser Ser				
	100	105		110
Ile Glu Lys Thr Ile Ser Xaa Ala Xaa Gly Gln Pro Arg Glu Pro Gln				
	115	120		125
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val				
	130	135		140
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val				
	145	150		155
				160

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 696 does not have a feature to cover the "Xaa" at positions 96, 106, 119 and 121. Please make all necessary changes.

Application No: 10627556 Version No: 2.0

Input Set:

Output Set:

Started: 2009-02-18 18:53:57.456
Finished: 2009-02-18 18:54:16.952
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 496 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

Input Set:

Output Set:

Started: 2009-02-18 18:53:57.456
Finished: 2009-02-18 18:54:16.952
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 496 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520)
W 251	Found intentionally skipped sequence in SEQID (521)
W 251	Found intentionally skipped sequence in SEQID (522)
W 251	Found intentionally skipped sequence in SEQID (523)
W 251	Found intentionally skipped sequence in SEQID (524)
W 251	Found intentionally skipped sequence in SEQID (525)
W 251	Found intentionally skipped sequence in SEQID (526)
W 251	Found intentionally skipped sequence in SEQID (527)
W 251	Found intentionally skipped sequence in SEQID (639)

Input Set:

Output Set:

Started: 2009-02-18 18:53:57.456
Finished: 2009-02-18 18:54:16.952
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 496 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640)
W 251	Found intentionally skipped sequence in SEQID (643)
W 251	Found intentionally skipped sequence in SEQID (646)
W 251	Found intentionally skipped sequence in SEQID (680)
W 251	Found intentionally skipped sequence in SEQID (681)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
W 251	Found intentionally skipped sequence in SEQID (688)
W 251	Found intentionally skipped sequence in SEQID (689)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 341	'Xaa' position not defined SEQID (696) POS (96)
E 341	'Xaa' position not defined SEQID (696) POS (106)
E 341	'Xaa' position not defined SEQID (696) POS (119)
E 341	'Xaa' position not defined SEQID (696) POS (121)
W 251	Found intentionally skipped sequence in SEQID (699)

<110> Ledbetter, Jeffrey A.

Hayden-Ledbetter, Martha

Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.401C2

<140> 10627556

<141> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> Homo sapiens

<400> 1

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atctcccgaa	ccctcgaggt	cacatgcgtg	gtggtggacg	tgagccacga	agaccctgag	180
gtcaagttca	actggtaacgt	ggacggcgtg	gaggtgcata	atgccaagac	aaagccgcgg	240
gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	300
tggctgaatg	gcaaggagta	caagtgcag	gtctccaaca	aagccctccc	agccccatc	360
gagaaaacaa	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	caccctgccc	420
ccatcccgaa	atgagctgac	caagaaccag	gtcagcctga	cctgcctgg	caaaggcttc	480
tatcccagcg	acatcgccgt	ggagtggag	agcaatggc	agccggagaa	caactacaag	540
accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gctcaccgtg	600
gacaagagca	ggtggcagca	gggaaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	660
cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtaaatgatc	taga	714

<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

Ser	Asp	Gln	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
1															15
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
					20				25				30		
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
							35		40				45		
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
							50		55				60		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
							65		70				75		80
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
							85		90				95		

Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
100							105					110			
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
115							120					125			
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
130				135						140					
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
145						150				155			160		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	165						170				175				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	180						185				190				
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
	195						200				205				
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
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Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
	225						230				235				

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actnccagga	ggcccttctg	tctttgtctt	ccccccgaaa	cccaaggacg	tcctctccat								120		
ttttggaggc	cgagtcacgt	gcgtttagt	ggacgtcgga	aagaaagacc	ccgagggtcaa								180		
tttcaactgg	tatattgtat	gcgtttaggt	gcgaacggcc	aatacgaagc	caaaaagagga								240		
acagttcaac	agcacgtacc	gcgtggtag	cgtcctgccc	atccagcacc	aggactggct								300		
gacggggaaag	gaattcaagt	gcaaggtcaa	caacaaagct	ctcccgcccc	ccatcgagag								360		
gaccatctcc	aaggccaaag	ggcagacccg	ggagccgcag	gtgtacaccc	tggccccaca								420		
ccgggaaagaa	ctggccaaagg	acaccgttag	cgtaacatgc	ctggtaaaag	gcttctaccc								480		
agctgacatc	aacgttgagt	ggcagaggaa	cggtcagccg	gagtccagagg	gcacactacgc								540		

caacacgccc	ccacagctgg	acaacgacgg	gacctacttc	ctctacagca	agctctcggt	600
gggaaagaac	acgtggcagc	ggggagaaac	cttaacctgt	gtggtgatgc	atgaggccct	660
gcacaaccac	tacaccaga	aatccatcac	ccagttcg	ggtaaatagt	aatctaga	718

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

Glu	Pro	His	Gly	Gly	Cys	Thr	Cys	Pro	Gln	Cys	Pro	Ala	Pro	Glu	Leu
1															
														15	
Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
														30	
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
														45	
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
														60	
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
														80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
														95	
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
														110	
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
														125	
Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr
														140	
Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ala	Asp	Ile	Asn
														160	
Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala
														175	
Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser
														190	
Arg	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Arg	Gly	Glu	Thr	Leu	Thr
														205	
Gly	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
														220	
Ile	Thr	Gln	Ser	Ser	Gly	Lys									
														230	

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

tgatcaagaa	cccaagacac	caaaaccaca	accacaacca	caaccacaac	ccaatcctac	60
aacagaatcc	aagtgtccca	aatgtccagc	ccctgagctc	ctgggagggc	cctcagtctt	120
catcttcccc	ccgaaaccca	aggacgtcct	ctccatttct	ggggaggccc	aggtcacgtg	180
cgttgtggta	gacgtgggccc	aggaagaccc	cgaggtcagt	ttcaactgg	acattgtatgg	240
cgcgtgggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgttaccg	300
cgttgtcagc	gtccctgccc	tccagcacca	ggactggctg	acggggaaagg	aattcaagt	360
caagggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagacccgg	gagccgcagg	tgtacaccct	ggccccacac	cgggaaagagc	tggccaagga	480
caccgtgagc	gtAACATGCC	ttgtcaaagg	cttctaccca	cctgatatac	acgttgagt	540
gcagaggaat	gggcagccgg	agtcaagagg	cacytacgcc	accacgcccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	ttgtgtatgc	cgaggccctg	cacaaccact	acacccagaa	720

<210> 6
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 <212> PRT
 <213> Lama glama
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Asp	Gln	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Gln		
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Pro	Asn	Pro	Thr	Thr	Glu	Ser	Lys	Cys	Pro	Lys	Cys	Pro	Ala	Pro	Glu
					20			25			30				
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
					35			40			45				
Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
					50			55			60				
Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	Asp	Gly
		65			70			75				80			
Ala	Glu	Val	Arg	Thr	Ala	Asn	Thr	Arg	Pro	Lys	Glu	Gln	Phe	Asn	
					85			90			95				
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp
					100			105			110				
Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro
					115			120			125				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu
					130			135			140				
Pro	Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp
	145				150				155			160			
Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	Asp	Ile
					165			170			175				
Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr
					180			185			190				
Ala	Thr	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr
					195			200			205				
Ser	Lys	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Gln	Gly	Glu	Thr	Phe
					210			215			220				
Thr	Cys	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	225				230				235			240			
Ser	Ile	Thr	Gln	Ser	Ser	Gly	Lys								
					245										

<210> 7
 <211> 727
 <212> DNA
 <213> Lama glama
 <400> 7

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actccttgg	ggggccacgg	tcttcatctt	ccccccgaaa	gccaaaggacg	tcctctccat	120
cacccgaaaa	cctgagggtca	cgtgcttgtg	gtggacgtgg	gtaaagaaga	ccctgagatc	180
gagttcaagc	tgggtccgtgg	atgacacaga	ggtacacacg	gctgagacaa	agccaaagga	240
ggaacagttc	aacagcacgt	accgcgtgg	cagcgtcctg	cccatccagc	accaggactg	300
gctgacgggg	aaggaatca	agtgcaggt	caacaacaaa	gctctccag	ccccccatcga	360
gaggaccatc	tccaaggcca	aaggcagac	ccggggagccg	caggtgtaca	ccctggcccc	420
acaccgggaa	gagctggcca	aggacaccgt	gagcgttaacc	tgcctggta	aaggcttctt	480
cccaagctgac	atcaacgttg	agtggcagag	gaatggcag	ccggagtcag	agggcaccta	540
cggccaaacacg	tggacaacga	cgggacctac	ttccctctaca	gcaaactctc		600
cgtggggaaag	aacacgtggc	agcagggaga	agtcttcacc	tgtgtggta	tgcacgaggc	660
tctacacaat	cactccacccc	agaaatccat	cacccagatc	tcgggtaaat	agtaatctag	720

<210> 8
 <211> 236
 <212> PRT
 <213> Lama glama
 <400> 8

Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys
 1 5 10 15
 Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
 20 25 30
 Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
 35 40 45
 Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Trp
 50 55 60
 Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
 65 70 75 80
 Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
 85 90 95
 His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 100 105 110
 Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
 115 120 125
 Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
 130 135 140
 Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
 145 150 155 160
 Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
 165 170 175
 Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
 180 185 190
 Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
 195 200 205
 Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
 210 215 220
 Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 225 230 235

<210> 9
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 <212> DNA
 <213> Homo sapiens
 <400> 9

gatcaggagc ccaaattcttg tgacaaaaact cacacatgcc caccgtgcc agca 54

<210> 10
 <211> 18
 <212> PRT
 <213> Homo sapiens
 <400> 10

Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 1 5 10 15
 Pro Ala

<210> 11
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<213> Homo sapiens
<400> 11
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<210> 12
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Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15
Pro Ala

<210> 13
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atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
gactggctga atggcaagga gtacaagtgc aaggcttcca acaaagccct cccagccccc 300
atcgagaaaa ccatctccaa agccaaa 327

<210> 14
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<212> PRT
<213> Homo sapiens
<400> 14
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35 40 45
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Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
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Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
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